

Appendix I: Alignment of the CMV IE enhancer of M60321 with instant SEQ ID NO: 3

BLASTN 2.2.25+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: N05YT4ZW111

Query= gi|330624|gb|M60321.1|HS5MIEP Human cytomegalovirus major immediate-early protein gene, 5' end

Length=2361

Sequences producing significant alignments:	Score (Bits)	E Value
lcl 26147 SID_3	977	0.0

ALIGNMENTS

>lcl|26147 SID_3

Length=3584

Score = 977 bits (529), Expect = 0.0
 Identities = 543/549 (99%), Gaps = 3/549 (0%)
 Strand=Plus/Plus

Query	535	ACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATT	594
Sbjct	29	ACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATT	88
Query	595	AGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATGGCCCGCTCG	654
Sbjct	89	AGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATGGCCCGCTCG	148
Query	655	-TGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATTGCCATAGTAAC	713
Sbjct	149	CTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATTGCCATAGTAGC	208
Query	714	GCCAAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCCACTT	773
Sbjct	209	GCCAAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCCACTT	268
Query	774	GGCAGTACATCAAGTGTATCATATGCCAAGTCCGGCCCTATTGACGTCAATGACGGTA	833
Sbjct	269	GGCAGTACATCAAGTGTATCATATGCCAAGTCC-GCCCCCTATTGACGTCAATGACGGTA	327
Query	834	AATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTTCTACTTGGCAGT	893
Sbjct	328	AATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTTCTACTTGGCAGT	387
Query	894	ACATCTACGTATTAGTCATCGCTATTACCATGGTG-ATCGGGTTTGGCAGTACACCAAT	952
Sbjct	388	ACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTGGCAGTACACCAAT	447
Query	953	GGGCGTGGATAGCGGTTTGACTCACGGGGATTTCGAAGTCCACCCCAATTGACGTCAAT	1012
Sbjct	448	GGGCGTGGATAGCGGTTTGACTCACGGGGATTTCGAAGTCCACCCCAATTGACGTCAAT	507

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Query 1013 GGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCCGCC 1072
          |||
Sbjct 508 GGGAGTTTGTGTTTGGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCCGCC 567

Query 1073 CCGTTGACG 1081
          |||
Sbjct 568 CCGTTGACG 576
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